



SEQUENCE LISTING

6 A

<110> Meyers, Rachael
Kapeller-Libermann, Rosana
Silos-Santiago, Immaculada

<120> 18431 AND 32374, NOVEL HUMAN PROTEIN
KINASE FAMILY MEMBERS AND USES THEREFOR

<130> 381552002700

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<141> 2001-07-27

<150> 60/221,543

<151> 2000-07-28

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gatctggtg	tetacaagg	cacaggcaca	aaa atg gca	ctg aag ttt	gtg aac	294
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			1	5		

aag agc aaa acc aag	ctg aag aac ttc	cta cgg gag	gtg agc atc acc	342
Lys Ser Lys Thr Lys Leu Lys Asn Phe Leu Arg Glu Val Ser Ile Thr				
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aac agc ctc tcc tcc agc ccc ttc atc atc aag gtc ttt gac gtg gtc	390		
Asn Ser Leu Ser Ser Ser Pro Phe Ile Ile Lys Val Phe Asp Val Val			
25	30	35	

ttt gag aca gag gac tgc tac gtc ttt gcc cag gag tac gca cct gct	438		
Phe Glu Thr Glu Asp Cys Tyr Val Phe Ala Gln Glu Tyr Ala Pro Ala			
40	45	50	55

ggg gac ctg ttt gac atc atc cct ccc cag gtg ggg ctc cct gag gac	486
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Gly Asp Leu Phe Asp Ile Ile Pro Pro Gln Val Gly Leu Pro Glu Asp	60	65	70	
acg gtg aag cgc tgt gtg cag cag ctg ggc ctg gcg ctg gac ttc atg	75	80	85	534
Thr Val Lys Arg Cys Val Gln Gln Leu Gly Leu Ala Leu Asp Phe Met				
cac ggg cgg cag ctg gtg cac cgc gac atc aag ccc gag aac gtg ctg	90	95	100	582
His Gly Arg Gln Leu Val His Arg Asp Ile Lys Pro Glu Asn Val Leu				
ctg ttc gac cgc gag tgc cgc cgc gta aag ctg gcc gac ttc ggc atg	105	110	115	630
Leu Phe Asp Arg Glu Cys Arg Arg Val Lys Leu Ala Asp Phe Gly Met				
acg cgc cgc gtg gcc tgc cgc gtc aag cgc gtg agc ggc acc atc cct	120	125	130	678
Thr Arg Arg Val Gly Cys Arg Val Lys Arg Val Ser Gly Thr Ile Pro				
tac acg gcg cct gag gtg tgc cag gcg ggc cgc gcc gac ggg ctg gcg	140	145	150	726
Tyr Thr Ala Pro Glu Val Cys Gln Ala Gly Arg Ala Asp Gly Leu Ala				
gtg gac acg ggc gtg gac gtg tgg gcc ttc ggc gtg ctc atc ttc tgc	155	160	165	774
Val Asp Thr Gly Val Asp Val Trp Ala Phe Gly Val Leu Ile Phe Cys				
gtg ctc acc ggc aac ttc cgg tgg gag gcg gcg tgg ggc gcc gac gcc	170	175	180	822
Val Leu Thr Gly Asn Phe Pro Trp Glu Ala Ala Ser Gly Ala Asp Ala				
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Phe Phe Glu Glu Phe Val Arg Trp Gln Arg Gly Arg Leu Pro Gly Leu				
cct tcg cag tgg cgc cgc ttc acc gag ccc gcg ctg cgc atg ttc cag	200	205	210	918
Pro Ser Gln Trp Arg Phe Thr Glu Pro Ala Leu Arg Met Phe Gln				
cgc tta ctg gcc ctg gag ccc gag cgc cgc ggc cca gcc aag gag gtg	220	225	230	966
Arg Leu Leu Ala Leu Glu Pro Glu Arg Arg Gly Pro Ala Lys Glu Val				
ttc cgc ttc ctc aag cac gag ctc acg tcc gag ctg cgc cgc cgg ccc	235	240	245	1014
Phe Arg Phe Leu Lys His Glu Leu Thr Ser Glu Leu Arg Arg Arg Pro				
tcg cac cgc gcg cgc aag ccc ccc ggg gac cgc ccg ccc gcc gcc ggg	250	255	260	1062
Ser His Arg Ala Arg Lys Pro Pro Gly Asp Arg Pro Pro Ala Ala Gly				
cca ctg cgc ctc gag gcg cct ggg ccg ctc aag cgg acg gtg ctg acc	265	270	275	1110
Pro Leu Arg Leu Glu Ala Pro Gly Pro Leu Lys Arg Thr Val Leu Thr				
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Glu Ser Gly Ser Gly Ser Arg Pro Ala Pro Pro Ala Val Gly Ser Val				

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Pro Leu Pro Val Pro Val Pro Val Pro Val Pro Val Pro Val Pro Val	300	305	310	
ccc gag ccc ggc cta get ccc cag ggg ccc ccc ggc cgg acc gac ggc				1254
Pro Glu Pro Gly Pro Gly Leu Ala Pro Gln Gly Pro Pro Gly Arg Thr Asp Gly	315	320	325	
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Arg Ala Asp Lys Ser Lys Gly Gln Val Val Leu Ala Thr Ala Ile Glu	330	335	340	
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Ile Cys Val *	345			
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Ile Lys Val Phe Asp Val Val Phe Glu Thr Glu Asp Cys Tyr Val Phe				
35 40 45				

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Gln Val Gly Leu Pro Glu Asp Thr Val Lys Arg Cys Val Gln Gln Leu
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Gly Leu Ala Leu Asp Phe Met His Gly Arg Gln Leu Val His Arg Asp
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Ile Lys Pro Glu Asn Val Leu Leu Phe Asp Arg Glu Cys Arg Arg Val
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Lys Leu Ala Asp Phe Gly Met Thr Arg Arg Val Gly Cys Arg Val Lys
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Arg Val Ser Gly Thr Ile Pro Tyr Thr Ala Pro Glu Val Cys Gln Ala
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Gly Arg Ala Asp Gly Leu Ala Val Asp Thr Gly Val Asp Val Trp Ala
145 150 155 160
Phe Gly Val Leu Ile Phe Cys Val Leu Thr Gly Asn Phe Pro Trp Glu
165 170 175
Ala Ala Ser Gly Ala Asp Ala Phe Phe Glu Glu Phe Val Arg Trp Gln
180 185 190
Arg Gly Arg Leu Pro Gly Leu Pro Ser Gln Trp Arg Arg Phe Thr Glu
195 200 205
Pro Ala Leu Arg Met Phe Gln Arg Leu Leu Ala Leu Glu Pro Glu Arg
210 215 220
Arg Gly Pro Ala Lys Glu Val Phe Arg Phe Leu Lys His Glu Leu Thr
225 230 235 240
Ser Glu Leu Arg Arg Arg Pro Ser His Arg Ala Arg Lys Pro Pro Gly
245 250 255
Asp Arg Pro Pro Ala Ala Gly Pro Leu Arg Leu Glu Ala Pro Gly Pro
260 265 270
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275 280 285
Pro Pro Ala Val Gly Ser Val Pro Leu Pro Val Pro Val Pro
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Val Pro Val Pro Val Pro Val Pro Glu Pro Gly Leu Ala Pro Gln Gly
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 Phe Phe Ala Ser Ala Leu Pro His Asp Val Cys Gly Ser Asn Gly Leu
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 cct ctg aca cca aat tcc atc aaa att tta ggg cgc ttt caa atc ctt 685
 Pro Leu Thr Pro Asn Ser Ile Lys Ile Leu Gly Arg Phe Gln Ile Leu
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 aaa acc atc acc cat ccc aga ctc tgc cag tat gtg gat att tct agg 733
 Lys Thr Ile Thr His Pro Arg Leu Cys Gln Tyr Val Asp Ile Ser Arg
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 gga aag cat gaa cga cta gtg gtc gtg gct gaa cat tgt gaa cgt agt 781
 Gly Lys His Glu Arg Leu Val Val Val Ala Glu His Cys Glu Arg Ser
 65 70 75

 ctg gaa gac ttg ctt cga gaa agg aaa cct gtg agc tgt tca acg gtt 829
 Leu Glu Asp Leu Leu Arg Glu Arg Lys Pro Val Ser Cys Ser Thr Val
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 ttg tgt ata gca ttt gag gtt ctt cag ggc ttg cag tat atg aac aaa 877
 Leu Cys Ile Ala Phe Glu Val Leu Gln Gly Leu Gln Tyr Met Asn Lys
 95 100 105

 cat ggt ata gta cac agg gca ttg tct cct cat aat atc ctg ttg gac 925
 His Gly Ile Val His Arg Ala Leu Ser Pro His Asn Ile Leu Leu Asp
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gct cat ggt gat gat gtt gat ttc cca ata ggg tat ccc tcg tac ttg Ala His Gly Asp Asp Val Asp Phe Pro Ile Gly Tyr Pro Ser Tyr Leu 145 150 155	1021
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670 675 680 685	
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Ile Pro Leu Asn Asp Leu Lys Ser Glu Val Ser Pro Arg Ile Ser Ala	
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Thr Pro Ser Lys Lys Thr Lys Ser Ser Lys Pro Lys Leu Leu Val Val	
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 830 835 840 845

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 865 870 875

aat aaa ata aag cca aca ggc ctc ctc acc atc cca tct cct caa ata 3229
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<210> 5
 <211> 893
 <212> PRT
 <213> Homo sapiens

<400> 5
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 20 25 30
 Pro Asn Ser Ile Lys Ile Leu Gly Arg Phe Gln Ile Leu Lys Thr Ile
 35 40 45
 Thr His Pro Arg Leu Cys Gln Tyr Val Asp Ile Ser Arg Gly Lys His
 50 55 60
 Glu Arg Leu Val Val Val Ala Glu His Cys Glu Arg Ser Leu Glu Asp

65	Leu	Leu	Arg	Glu	Arg	Lys	Pro	Val	Ser	Cys	Ser	Thr	Val	Leu	Cys	Ile	80
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Ala	Phe	Glu	Val	Leu	Gln	Gly	Leu	Gln	Tyr	Met	Asn	Lys	His	Gly	Ile		
			100						105					110			
Val	His	Arg	Ala	Leu	Ser	Pro	His	Asn	Ile	Leu	Leu	Asp	Arg	Lys	Gly		
			115				120						125				
His	Ile	Lys	Leu	Ala	Lys	Phe	Gly	Leu	Tyr	His	Met	Thr	Ala	His	Gly		
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Asp	Asp	Val	Asp	Phe	Pro	Ile	Gly	Tyr	Pro	Ser	Ser	Tyr	Leu	Ala	Pro	Glu	
			145		150					155						160	
Val	Ile	Ala	Gln	Gly	Ile	Phe	Lys	Thr	Thr	Asp	His	Met	Pro	Ser	Lys		
			165						170						175		
Lys	Pro	Leu	Pro	Ser	Gly	Pro	Lys	Ser	Asp	Val	Trp	Ser	Leu	Gly	Ile		
			180					185					190				
Ile	Leu	Phe	Glu	Leu	Cys	Val	Gly	Arg	Lys	Leu	Phe	Gln	Ser	Leu	Asp		
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Ile	Ser	Glu	Arg	Leu	Lys	Phe	Leu	Leu	Thr	Leu	Asp	Cys	Val	Asp	Asp		
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Thr	Leu	Ile	Val	Leu	Ala	Glu	Glu	His	Gly	Cys	Leu	Asp	Ile	Ile	Lys		
			225		230					235							
Glu	Leu	Pro	Glu	Thr	Val	Ile	Asp	Leu	Leu	Asn	Lys	Cys	Leu	Thr	Phe		
			245					250						255			
His	Pro	Ser	Lys	Arg	Pro	Thr	Pro	Asp	Glu	Leu	Met	Lys	Asp	Lys	Val		
			260					265						270			
Phe	Ser	Glu	Val	Ser	Pro	Leu	Tyr	Thr	Pro	Phe	Thr	Lys	Pro	Ala	Ser		
			275					280				285					
Leu	Phe	Ser	Ser	Ser	Leu	Arg	Cys	Ala	Asp	Leu	Thr	Thr	Leu	Pro	Glu	Asp	
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Ile	Ser	Gln	Leu	Cys	Lys	Asp	Ile	Asn	Asn	Asp	Tyr	Leu	Ala	Glu	Arg		
			305		310					315							
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Glu	Lys	Glu	Leu	Val	Asn	Lys	Glu	Ile	Ile	Arg	Ser	Lys	Pro	Pro	Ile		
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Gly	Arg	Asp	Arg	Ser	Ser	Leu	Leu	Asp	Asp	Thr	Thr	Val	Thr	Leu	Ser		
			370		375							380					
Leu	Cys	Gln	Leu	Arg	Asn	Arg	Leu	Lys	Asp	Val	Gly	Gly	Glu	Ala	Phe		
			385		390					395					400		

Arg Arg Val Leu Lys Ala Trp Val Val Ser His Pro Asp Leu Val Tyr
 530 535 540
 Trp Gln Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Tyr Leu Asn Phe
 545 550 555 560
 Asn Asn Glu Ala Leu Ala Tyr Ala Cys Met Ser Ala Phe Ile Pro Lys
 565 570 575
 Tyr Leu Tyr Asn Phe Phe Leu Lys Asp Asn Ser His Val Ile Gln Glu
 580 585 590
 Tyr Leu Thr Val Phe Ser Gln Met Ile Ala Phe His Asp Pro Glu Leu
 595 600 605
 Ser Asn His Leu Asn Glu Ile Gly Phe Ile Pro Asp Leu Tyr Ala Ile
 610 615 620
 Pro Trp Phe Leu Thr Met Phe Thr His Val Phe Pro Leu His Lys Ile
 625 630 635 640
 Phe His Leu Trp Asp Thr Leu Leu Leu Gly Asn Ser Ser Phe Pro Phe
 645 650 655
 Cys Ile Gly Val Ala Ile Leu Gln Gln Leu Arg Asp Arg Leu Leu Ala
 660 665 670
 Asn Gly Phe Asn Glu Cys Ile Leu Leu Phe Ser Asp Leu Pro Glu Ile
 675 680 685
 Asp Ile Glu Arg Cys Val Arg Glu Ser Ile Asn Leu Phe Cys Trp Thr
 690 695 700
 Pro Lys Ser Ala Thr Tyr Arg Gln His Ala Gln Pro Pro Lys Pro Ser
 705 710 715 720
 Ser Asp Ser Ser Gly Gly Arg Ser Ser Ala Pro Tyr Phe Ser Ala Glu
 725 730 735
 Cys Pro Asp Pro Pro Lys Thr Asp Leu Ser Arg Glu Ser Ile Pro Leu
 740 745 750
 Asn Asp Leu Lys Ser Glu Val Ser Pro Arg Ile Ser Ala Glu Asp Leu
 755 760 765
 Ile Asp Leu Cys Glu Leu Thr Val Thr Gly His Phe Lys Thr Pro Ser
 770 775 780
 Lys Lys Thr Lys Ser Ser Lys Pro Lys Leu Leu Val Asp Ile Arg
 785 790 795 800
 Asn Ser Glu Asp Phe Ile Arg Gly His Ile Ser Gly Ser Ile Asn Ile
 805 810 815
 Pro Phe Ser Ala Ala Phe Thr Ala Glu Gly Glu Leu Thr Gln Gly Pro
 820 825 830
 Tyr Thr Ala Met Leu Gln Asn Phe Lys Gly Lys Val Ile Val Ile Val
 835 840 845
 Gly His Val Ala Lys His Thr Ala Glu Phe Ala Ala His Leu Val Lys
 850 855 860
 Met Lys Tyr Pro Arg Ile Cys Ile Leu Asp Gly Gly Ile Asn Lys Ile
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<210> 6
 <211> 2692
 <212> DNA
 <213> Homo sapiens

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 cgctttcaaa tctttaaac catcaccat cccagactct gccagtatgt ggatattct 180
 aggggaaagc atgaacgact agtggctcgt gctgaacatt gtgaacgtag tctggaagac 240

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aatatcctgt	tggaccgaaa	gggacatatt	aaatttggcta	aattttgact	ttatcacatg	420
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gtaattgcac	agggaaat	caaaaccact	gatcacatgc	caagtataaaa	accattgcct	540
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gcaattcttc	agcagctcgc	ggaccggcct	ttggctaagt	gctttaaata	gtgtattctt	2040
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caccttgtga	agatgaaata	tccaagaatc	tgtattctag	atgggtggcat	taataaaaata	2640
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<210> 7

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 7

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Gln	Ile	Leu	Lys	Arg	Leu	Ser	His	Pro	Asn	Ile	Val	Arg	Leu	Leu	Gly
			20					25					30		
Val	Phe	Glu	Asp	Thr	Asp	Asp	His	Leu	Tyr	Leu	Val	Met	Glu	Tyr	Met
	35						40					45			

Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Pro Leu Ser
 50 55 60
 Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu
 65 70 75 80
 Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn
 85 90 95
 Ile Leu Leu Asp Glu Asn Gly Thr Val Lys Ile Ala Asp Phe Gly Leu
 100 105 110
 Ala Arg Leu Leu Glu Lys Leu Thr Thr Phe Val Gly Thr Pro Trp Tyr
 115 120 125
 Met Met Ala Pro Glu Val Ile Leu Glu Gly Arg Gly Tyr Ser Ser Lys
 130 135 140
 Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Glu Leu Leu Thr Gly
 145 150 155 160
 Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro Ala Phe Thr Gly Gly Asp
 165 170 175
 Glu Val Asp Gln Leu Ile Ile Phe Val Leu Lys Leu Pro Phe Ser Asp
 180 185 190
 Glu Leu Pro Lys Thr Arg Ile Asp Pro Leu Glu Glu Leu Phe Arg Ile
 195 200 205
 Lys Lys Arg Arg Leu Pro Leu Pro Ser Asn Cys Ser Glu Glu Leu Lys
 210 215 220
 Asp Leu Leu Lys Lys Cys Leu Asn Lys Asp Pro Ser Lys Arg Pro Gly
 225 230 235 240
 Ser Ala Thr Ala Lys Glu Ile
 245

<210> 8

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 8

Gly Pro Ala Lys Glu Val Phe Arg Phe Leu Lys His Glu Leu Thr Ser
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 Glu Leu Arg Arg Arg Pro Ser His Arg Ala Arg Lys Pro Pro Gly Asp
 20 25 30
 Arg Leu Pro Gly Pro Leu Arg Leu Glu Ala Pro Gly Pro Leu Lys Arg
 35 40 45
 Thr Val Leu Thr Glu Ser Gly Ser Gly Ser Arg
 50 55

<210> 9

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 9

Pro Pro Gly Arg Thr Asp Gly Arg Ala Asp Lys Ser Lys Gly Gln Val
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 Val Leu Ala Thr Ala Ile Glu Ile Cys Val

<210> 10
 <211> 80
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 10
 Tyr Cys Met Lys Gly Lys Phe Pro Trp Gln Lys Ala Ser Ile Met Cys
 1 5 10 15
 Lys Pro Tyr Trp Glu Trp Glu Gln Trp Leu Lys Arg Lys Asn Pro Ala
 20 25 30
 Leu Pro Lys Lys Phe Asn Pro Phe Ser Glu Lys Ala Leu Lys Leu Phe
 35 40 45
 Lys Lys Ser Leu Thr Pro Arg Phe Lys Asp Arg Trp Thr Ala Lys Asp
 50 55 60
 Met Arg Lys Cys Leu Ala Lys Glu Lys Leu Leu Lys Ser Val Lys Arg
 65 70 75 80

<210> 11
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 11
 Lys Met Val Ala Phe Ser Lys Arg Glu Glu Glu Arg Ile Leu Leu Glu
 1 5 10 15
 Ile Asp Leu Tyr Lys Lys Leu Glu Asn Glu Phe Val Ile Asp Leu
 20 25 30
 Met Ala His Ile Val Asp Asp Ile Thr His Tyr Leu Leu Phe Asp Lys
 35 40 45
 Tyr Ser Gln Asn Phe Leu Glu Tyr Ile Glu Glu Leu Lys Ile Gly Gly
 50 55 60
 Glu Val Asp Glu Leu Lys His Leu Lys Tyr Phe Ser Gly Ile Val Ser
 65 70 75 80
 Ala Ile Glu Gln Leu His Gly Phe Glu Phe Ala His Leu Asp Ile Lys
 85 90 95
 Pro Ala Asn Ile Leu Lys Ser Gly Asp Thr Ile Lys Met Ile Asp Phe
 100 105 110
 Gly

<210> 12
 <211> 142
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 12

Met Ile Ala Leu Glu Trp Leu Pro Gly Gly Thr Leu Ala Asp Tyr Phe
 1 5 10 15
 Gln Phe Lys Val Arg Glu Lys Asp Asp Ser Glu Arg Ser Pro Ile Gln
 20 25 30
 Leu Lys Asp Met Leu Ser Ile Leu Tyr Gln Val Ser Gln Ala Leu Lys
 35 40 45
 Tyr Ile His Ser Gln Leu Asp Glu Phe Gly Gln Glu Thr His Gly
 50 55 60
 Arg Ile Phe Thr Arg Asn Val Leu Val Thr Glu Pro Asp Leu Arg Lys
 65 70 75 80
 Cys Glu Val Lys Leu Gly Asp Phe Gly Asp Ala Pro Met Gly Leu Glu
 85 90 95
 Tyr Ser Thr Pro Ile Ile Ala Tyr Met Pro Pro Glu Ile Leu Cys Cys
 100 105 110
 Ala Glu Arg Ile Pro Pro His Arg Pro Glu Asn Asp Val Trp Met Phe
 115 120 125
 Gly Val Phe Ile Trp Glu Cys Leu Thr Leu Gly Ala Gln Pro
 130 135 140

<210> 13
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 13
 Ile Ala Gln Leu Leu Glu Ala Cys Thr Tyr Leu His Lys His Lys Val
 1 5 10 15
 Ala Gln Arg Asp Met Lys Ser Asp Asn Ile Leu Leu Glu Tyr Asp Phe
 20 25 30
 Asp Asp Glu Ile Pro Gln Leu Val Val Ala Asp Phe Gly Cys Ala Leu
 35 40 45
 Ala Cys Asp Asn Trp Gln Val Asp Tyr Glu Ser Asp Glu Val Ser Leu
 50 55 60
 Gly Gly Asn Ala Lys Thr Lys Ala Pro Glu Ile Ala Thr Ala Val Pro
 65 70 75 80
 Gly Lys Asn Val Lys Val Asn Phe Glu Met Ala Asp Thr Trp Ala Ala
 85 90 95
 Gly Gly Leu Ser Tyr Glu Val Leu Thr Arg Ser Asn Pro Phe Tyr Lys
 100 105 110
 Leu Leu Asp Thr Ala Thr Tyr Gln Glu Ser Glu Leu Pro Ala Leu Pro
 115 120 125
 Ser Arg
 130

<210> 14
 <211> 196
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 14
 Leu Pro Val Asp Gln Leu Glu Ala Tyr Gly Asp Tyr Leu Phe Gly Ala

1 5 10 15
 Val Asp Phe Leu Glu Gly Glu Gly Ile Trp His Arg Asp Ile Lys Pro
 20 25 30
 Asp Asn Ile Ala Val Arg Ile Arg Pro Asn Arg Thr Arg Glu Leu Val
 35 40 45
 Leu Ile Asp Phe Ser Leu Ala Gly Tyr Pro Ala Lys Asn Thr Asp Ala
 50 55 60
 Gly Thr Asp Gly Tyr Leu Asp Pro Phe Val Asp Val Ile Thr Arg Gly
 65 70 75 80
 Ser Tyr Asp Ser His Ala Glu Arg Tyr Ala Val Ala Val Thr Leu His
 85 90 95
 Gln Met Ala Ser Gly Glu Leu Pro Lys Trp Gly Asp Gly Ser Val Leu
 100 105 110
 Pro Arg Met Thr Asp Pro Lys Glu Trp Pro Tyr Pro Thr Ile Ala Ala
 115 120 125
 Glu Ala Phe Asp Pro Ala Val Arg Asp Gly Leu Val Ala Phe Phe Gln
 130 135 140
 Lys Ala Leu His Arg Asp Ala Gly Lys Arg Phe Pro Glu Leu Lys Pro
 145 150 155 160
 Met Arg Asp Ala Trp Arg Lys Val Phe Leu Asp Ala Ser Gln Thr Val
 165 170 175
 Pro Ser Ser His Arg Thr Arg Pro Ala Ala Pro Ala Asp Gly Ala Ala
 180 185 190
 Pro Ala Glu Gly
 195

<210> 15

<211> 170

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 15

Pro Gly Ile Leu Ala Ile Glu Asn Val Ser Glu Glu Glu Asp Arg Cys
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 Phe Leu Val Thr Gln Glu Asn Asp Gly Pro Ile Leu Ser Leu Thr Gln
 20 25 30
 Tyr Leu Lys Gly Ile Pro Arg Lys Leu Thr Glu Glu Glu Ile Val Asp
 35 40 45
 Ile Ile Gln Gln Leu Cys Ser Leu Leu Asp Tyr Val His Ser Glu Gly
 50 55 60
 Leu Ala His Gly Gln Trp Asn Leu His Ser Val His Ile His Phe Leu
 65 70 75 80
 Asn Gly Val Pro Asn Ile Tyr Leu Pro Asp Leu Gly Phe Ala Ser Leu
 85 90 95
 Ile Arg Glu Arg Met Phe Asp Gly Phe Met Gln Asp Glu Glu Asn Arg
 100 105 110
 Glu Ser Ile Glu Lys Ile Arg Asp Arg Leu Leu Phe His Thr Pro Glu
 115 120 125
 Gly Lys Gln Thr Asn Gly Arg Glu Thr Asp Thr Tyr Ala Phe Gly Ala
 130 135 140
 Ile Thr Tyr Tyr Leu Leu Phe Gly Phe Phe Pro Trp Gly Ile Phe Pro
 145 150 155 160
 Lys Pro Ser Lys Cys Phe Pro Asp Phe Ile
 165 170

<210> 16
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 16
 Ser Pro His Val Leu Pro Val Arg Asp Leu Ile Asp Glu Gly Glu Trp
 1 5 10 15
 Leu Ser Leu Val Phe Glu Pro Arg Arg Thr Ile Thr Leu Arg Glu Leu
 20 25 30
 Leu Ser Ala Gly Pro Val Ser Pro Glu Leu Leu Gln Pro Leu Thr Thr
 35 40 45
 Ala Leu Phe Glu Gly Leu Ser Ala Ala His Gln Gly Ala Leu Leu His
 50 55 60
 Thr Gln Ile Ser Pro Glu Ala Val Trp Phe Asp Thr Gln Lys Arg Pro
 65 70 75 80
 Leu Leu Ala Glu Phe Gly Leu Ala Arg Arg Thr Ala Gln Glu Leu Arg
 85 90 95
 Asp His Trp Pro His Asp Pro Arg Tyr Ala Ala Pro Glu Leu Leu Ser
 100 105 110
 Gly Gly Pro Tyr Thr Pro Gln Thr Asp Leu Tyr Ala Leu Ala Ala Thr
 115 120 125
 Leu Leu Glu Ala Ala Thr Gly Thr Ala Leu Ser Pro Val Ser Ala Arg
 130 135 140
 Gln Gln Gly Val Arg Leu Pro Ser Trp Pro Ala Gly Ile Pro Pro Gln
 145 150 155 160
 Val Ala His Ala Leu Glu Ser Cys Leu Gln Leu Asp Pro Ala Val Arg
 165 170 175
 Ala Val Ser Ala Ala Glu Val Leu Glu Glu Leu Arg Arg Ala Gln Pro
 180 185 190
 Thr Gln Ala Ile Leu Ser Gln Gln Glu Pro Pro Ala Pro Pro Ser
 195 200 205
 Val Pro Ser Pro Pro Ala Ala
 210 215

<210> 17
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 17
 Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Leu Gly
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 Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr Met
 20 25 30
 Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Pro Leu Ser
 35 40 45
 Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu
 50 55 60
 Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn

65 70 75 80
 Ile Leu Leu Asp Glu Asn Gly Thr Val Lys Ile Ala Asp Phe Gly Leu
 85 90 95
 Ala Arg Leu Leu Glu Lys Leu Thr Thr Phe Val Gly Thr Pro Trp Tyr
 100 105 110
 Met Met Ala Pro Glu Val Ile Leu Glu Gly Arg Gly Tyr Ser Ser Lys
 115 120 125
 Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Glu Leu Leu Thr Gly
 130 135 140
 Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro Ala Phe Thr Gly Gly Asp
 145 150 155 160
 Glu Val Asp Gln Leu Ile Ile Phe Val Leu Lys Leu Pro Phe Ser Asp
 165 170 175
 Glu Leu Pro Lys Thr Arg Ile Asp Pro Glu Glu Leu Phe Arg Ile
 180 185 190
 Lys Lys Arg Arg Leu Pro Leu Pro Ser Asn Cys Ser Glu Leu Lys
 195 200 205
 Asp Leu Leu Lys Lys Cys Leu Asn Lys Asp Pro Ser Lys Arg Pro Gly
 210 215 220
 Ser Ala Thr Ala Lys Glu Ile Leu Asn His Pro Trp Phe
 225 230 235

<210> 18
 <211> 341
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 18
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 Leu Leu Gly Ala Gln Glu Leu Asn Asn Cys Leu Leu Thr Asp Asn Phe
 20 25 30
 Lys Gly Leu Asp Leu Phe Gly Leu Val Pro Val Leu Leu Leu Ala Asp
 35 40 45
 Lys Asp Glu Tyr Glu Glu Leu Leu Asn Lys Asn Lys Glu Lys Thr Val
 50 55 60
 Gln Asp Gln Asn Glu Lys Ser Ser Val Gly Ile Arg Arg Leu Asp Tyr
 65 70 75 80
 Val Glu Ala Val Glu Lys His Pro Leu Ser Asp Asn Asp Lys Thr
 85 90 95
 Lys Gly Ser Leu Glu Lys Gly Ser Asp Glu Lys Ala Leu Lys Leu Arg
 100 105 110
 Glu Asp Leu Asp Lys Ile Glu Lys Asp Leu Ser Arg Thr Phe Pro Asp
 115 120 125
 Glu Ile Phe Phe Gln Thr Arg Leu Ala Glu Gln Gln Leu Lys Lys Asp
 130 135 140
 Gln Asp Leu Asp Ala Tyr Asp Lys Asp Glu Phe Asp Asp Glu Asp Asp
 145 150 155 160
 Lys Asn Glu Pro Pro Ser Ile Lys Gln Leu Arg Arg Leu Leu Val Ala
 165 170 175
 Tyr Ser Trp Lys Asn Pro Gln Glu His Leu Gly Tyr Val Gln Gly Met
 180 185 190
 Asn Val Ile Leu Ser Pro Leu Leu Phe Leu Lys His Gly Val Asp
 195 200 205

Leu Asp Glu Ile Asp Glu Glu Gln Ala Phe Trp Cys Leu Val Lys Leu
 210 215 220
 Met Asp Asn Tyr Leu Pro Gln Lys Tyr Phe Leu Asn Asp Leu Ser Gly
 225 230 235 240
 Leu Asn Glu Asp Leu Arg Val Leu Asp Ser Leu Val Lys Glu Ser Leu
 245 250 255
 Pro Glu Leu Tyr Ser His Leu Lys Lys Lys Glu Asn Lys Thr Gly Ser
 260 265 270
 Gly Lys Lys Lys Asn Leu Leu Ala Leu Asp Leu Thr Leu Leu Ile Phe
 275 280 285
 Ala Phe Pro Trp Phe Leu Thr Leu Phe Ala Arg Glu Leu Pro Leu Glu
 290 295 300
 Ile Val Leu Arg Ile Trp Asp Ile Leu Phe Thr Tyr Tyr Leu Gly Ser
 305 310 315 320
 His Phe Leu Ile Phe Val Ala Leu Ala Ile Leu Lys Leu Leu Lys Ser
 325 330 335
 Lys Leu Leu Lys His
 340

<210> 19
 <211> 170
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 19
 Ile Gln Arg Glu Thr Asn Ile Asp Val Pro Pro Thr Leu Arg Gly Glu
 1 5 10 15
 Val Trp Gly Cys Leu Leu Arg Val Pro Ser Ala Arg Thr Arg Tyr
 20 25 30
 Ala Leu Leu Asp His Ala Val His His Thr Ala Ala Lys Pro Thr Pro
 35 40 45
 His Asp Arg Gln Leu Glu Val Asp Ile Pro Arg Cys His Gln Tyr His
 50 55 60
 Pro Leu Leu Asn Ser Pro Ser Gly Ser Ala Gln Leu Arg Arg Ile Leu
 65 70 75 80
 Lys Ala Trp Gln Ile Val Tyr Leu Arg Pro Glu His Val Tyr Trp Gln
 85 90 95
 Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Thr Val Asn Asn Arg Asp
 100 105 110
 Glu Ala Leu Ala Phe Ala Gln Leu Asn Ala Phe Val Asn Arg Tyr Ile
 115 120 125
 His Trp Phe Tyr Leu Lys Asp Asn Ser Glu Val Ile Lys Glu Tyr Leu
 130 135 140
 Gly Lys Phe Tyr His Leu Thr Ala Tyr His Asp Pro Leu Leu Tyr Gln
 145 150 155 160
 His Leu Lys Ile Asn Gly Phe Asp Pro Glu
 165 170

<210> 20
 <211> 174
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 20

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Asn Gly Leu Pro Leu Thr Pro Pro Ala Lys Gln Met Leu Gly Arg Phe
 1           5           10           15
Pro Tyr Leu Gln Glu Leu Gln His Asp His Leu Cys Gln Tyr Leu His
 20           25           30
Phe Ile Arg Gly Lys His Glu Arg Asp Leu Thr Ile Val Val Met Glu
 35           40           45
His Tyr Gly Met Asn Leu Glu Asp Tyr Ala Lys Arg His Pro Pro Lys
 50           55           60
Asp Glu Ala Gln Asn Asn Asn Phe Tyr Tyr Gln Ile Ala Cys Gly Ile
 65           70           75           80
Asn Tyr Leu His Arg His His Ile Val His His Asn Leu His Pro Asn
 85           90           95
His Ile Tyr Ile Thr Asp Asp Gly Asn Arg Lys Leu Ser Val Lys Leu
100           105           110
Phe Asn Tyr Gly Leu His His Met Thr Asn Tyr Gly Lys Tyr Thr Pro
115           120           125
Phe Pro Ile Gly Asn Gly Arg Tyr Met Ala Pro Glu Arg Ile Leu Asn
130           135           140
Asp Asn Asp Asn Leu Phe Ala Ala Thr Tyr Gln Ser Asp Val Trp Glu
145           150           155           160
Leu Gly Phe Ile Met Leu Gln Ile Tyr Leu Gly Ile Glu Leu
165           170

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<210> 21

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 21

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Leu Ser Gln Ile Tyr His Leu Trp Gln Leu Ala Gly Gly Asp Val Gln
 1           5           10           15
Ala Glu Leu Lys Lys Glu Gly Leu Ile Arg Ser Glu Ala Pro Ile Leu
 20           25           30
Gly Leu Pro Gln Ile Val Arg Leu Ser Gly Ala Ser Val Cys Pro Gly
 35           40           45
Arg Ser Gln Ala Gln Leu Met Asp Asp Arg Val Val Pro Leu Arg Leu
 50           55           60
Lys Ala Leu Leu Gln Arg Leu Ser Gly Leu Pro Ala Ala Val Tyr Phe
 65           70           75           80
Pro Leu Leu His Ser Pro Arg Phe Pro Ala His Phe Ala Arg Glu Leu
 85           90           95
Gln Glu Leu Pro Leu Val Ile Arg Glu Lys Asp Ile Glu Tyr Gln Phe
100           105           110
Gln Arg Val Arg Leu Phe Ala Arg Leu Leu Gln Gly Tyr Pro His Thr
115           120           125
Ala Glu Gln
130

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<210> 22

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 22

Leu Lys Leu Ser Asn Val Val Arg Lys Ile Leu Ala Phe Gly Lys Ser
1 5 10 15
Asn Gly Ala Leu Glu Lys Ile Ala Arg Glu His Gln Cys His Glu Arg
20 25 30
Tyr Val Gln Met Asp Gln Arg Leu Arg Gln Leu Leu Glu Ser Cys Leu
35 40 45
Ser Val Leu Pro Lys Arg Arg Pro Leu Pro Gly Glu Leu Leu Glu His
50 55 60
Pro Ile Phe Glu Glu Val
65 70

<210> 23

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 23

Pro Leu Ser Gln Ile Tyr His Leu Trp
1 5

<210> 24

<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 24

Leu Tyr Ala Phe Gln Trp Phe Leu Thr Leu Phe Ala Arg Glu Leu Pro
1 5 10 15
Leu Glu Thr Val Leu Arg Ile Trp Asp Cys Phe Phe Tyr Glu Gly Ser
20 25 30
Lys Ile Leu Phe Arg Val Ala Leu Ala Leu Lys Met His Lys Glu
35 40 45
Glu Leu Leu Gln Ala Asp Asp Phe Glu Glu Met Leu Glu Phe Leu Gln
50 55 60
Asn Met Leu Pro Lys Arg Tyr Arg Ser Glu Glu Asp Ala Arg Arg Leu
65 70 75 80
Leu Glu Glu Ala Cys Asn Ile
85

<210> 25

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 25

Glu Met Met Glu Lys Leu Gln Lys Gln Ser Met Ser Glu Lys Lys Met
1 5 10 15
Glu Glu Met Ser Trp Val Ser Gln Leu Met Lys Ile Ala Tyr Gln Ile
20 25 30
Ala Lys Gly Leu Glu Tyr Leu His Ser Lys Ser Asn Lys Gln Asn Ile
35 40 45
Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Asn Asn Met
50 55 60
Val Ala Lys Gly Asp Ser Glu Ile Lys Val Val Lys Ile Ala Asp Phe
65 70 75 80
Gly Leu Ala Arg Met
85

<210> 26

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 26

Gly Thr Pro Ser Tyr Val Lys Tyr Val Gly Thr Arg Trp Tyr Met Ala
1 5 10 15
Pro Glu Val Leu Met Gly Ser Ser Tyr Gly Gln Tyr Ser Glu Lys Ser
20 25 30
Asp Val Trp Ser Phe Gly Val Ile Leu Tyr Glu Leu Leu Thr Gly Lys
35 40 45
Pro Pro Phe Phe Pro Gly Ser Ser Glu Val Asn Asp Ser Gln Met Asn
50 55 60
Glu Ile Met Lys Glu Thr Met Val Lys Ser Ala Glu Tyr Glu Met Pro
65 70 75 80
Met Lys Met Pro Met Pro Glu Ser Ser Lys Glu Ser Met Ser Cys Pro
85 90 95
Ser Met Ser Ser Glu Ala Val Lys Asp Leu Ile Lys Lys Cys Trp Gln
100 105 110
Lys Asp Pro Glu Lys Arg Pro Thr Phe Ala Gln Val Val Glu Glu Leu
115 120 125
Ser Ala His Glu Ile
130

<210> 27

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 27

Pro Pro Gln Ala Leu Asp Ile Gly Val Ala Asp Val Glu Leu Lys His
1 5 10 15
Leu Gln Gln Glu Gln Cys Pro Arg Ile Ser Ala Lys Asp Val Gln Phe
20 25 30

Leu Leu Asp Asn Ser Pro Ala Glu Leu Ala Leu Ile Asp Leu Arg Ser
 35 40 45
 Val Val Glu Phe Gly Arg Val His Val Pro His Ser Ile Asn Ile Pro
 50 55 60
 Phe Ala Thr Val Gln Leu Gly Glu Gln Arg Leu Glu Ala Leu Gln Val
 65 70 75 80
 Pro Gln Leu Glu Ala Gln Leu Arg Gly Lys Ile Val Val Cys Val Ser
 85 90 95
 Asn Ile His Gln His Ser Val Glu Val Gly His Pro Leu Ala Gln Leu
 100 105 110
 Lys

<210> 28
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 28
 Cys Val Leu Glu Ser Gln Lys Met Tyr Glu Ala Thr Pro Lys Ser Ile
 1 5 10 15
 Thr His Arg Gln His Ala Leu Arg Leu Gln Pro Pro Gln Ala Leu Asp
 20 25 30
 Ile Gly Val Ala Asp Val Glu Leu Lys His Leu Gln Gln Glu Gln Cys
 35 40 45
 Pro Arg Ile Ser Ala Lys Asp Val Gln Phe Leu Leu Asp Asn Ser Pro
 50 55 60
 Ala Glu Leu Ala Leu Ile Asp Leu Arg Ser Val Val Glu Phe Gly Arg
 65 70 75 80
 Val His Val Pro His Ser Ile Asn Ile Pro Phe Ala Thr Val
 85 90

<210> 29
 <211> 35
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 29
 Ser Gln Phe Ser His Phe Leu Val Ala Cys Gly Val Gln Arg Thr Cys
 1 5 10 15
 Ile Leu His Lys Gly Phe Asn Val Leu His Ser Ile Glu Pro Asn Ile
 20 25 30
 Leu Ile Ser
 35

<210> 30
 <211> 148
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 30
 Asp Thr Asp Ile Gly Gly Cys Phe Glu Tyr Asn Thr Phe Pro Pro Pro
 1 5 10 15
 Gly Lys Tyr Tyr Arg Gly Lys Leu Gly Leu Glu Glu Tyr Ala Val Phe
 20 25 30
 Tyr Pro Pro Asn Gly Val Ile Pro Phe His Gly Phe Cys Met Tyr Ala
 35 40 45
 Ala Pro Phe Cys Tyr Leu Tyr His Glu Pro Ser Lys Leu Tyr Tyr Thr
 50 55 60
 Phe Arg Glu Phe Tyr Ile Arg Tyr Cys His Arg Leu His Thr Ile Asn
 65 70 75 80
 Thr His Pro Gln Gly Ile Val Ser Leu Cys Leu Leu Phe Glu Lys Leu
 85 90 95
 Leu Gln Thr Tyr Glu Pro Gln Leu Trp Tyr His Phe Arg Glu Ile Gly
 100 105 110
 Ala Gln Pro Leu Arg Ile Ser Phe Lys Trp Met Met Arg Ala Phe Ser
 115 120 125
 Gly His Leu Pro Pro Asp Gln Leu Leu Leu Leu Trp Asp Arg Ile Leu
 130 135 140
 Gly Tyr Asn Ser
 145

<210> 31
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 31
 Ser Ala Ser Gln Leu Leu Arg Thr Tyr Phe Pro Glu Gly Met Ser Glu
 1 5 10 15
 Thr Leu Ile Arg Asn Ile Leu Phe Gly Ala Val Arg Gly Leu Asn Tyr
 20 25 30
 Leu His Gln Asn Gly Cys Ile His Arg Ser Ile Lys Ala Ser His Ile
 35 40 45
 Leu Ile Ser Gly Asp Gly Leu Val Thr Leu Ser Gly Leu Ser His Leu
 50 55 60
 His Ser Leu Val Lys His Gly Gln Arg His Arg Ala Val Tyr Asp Phe
 65 70 75 80
 Pro Gln Phe Ser Thr Ser Val Gln Pro Trp Leu Ser Pro Glu Leu Leu
 85 90 95
 Arg Gln Asp Leu His Gly Tyr Asn Val Lys Ser Asp Ile Tyr Ser Val
 100 105 110
 Gly Ile Thr Ala Cys Glu Leu Ala Ser Gly Gln Val Pro Phe Gln Asp
 115 120 125
 Met His Arg Thr Gln Met Leu
 130 135

<210> 32
 <211> 37
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 32

Lys Thr Phe Ser Pro Ala Phe Phe Ser Leu Val Gln Leu Cys Leu Gln
1 5 10 15
Gln Asp Pro Glu Lys Arg Pro Ser Ala Ser Ser Leu Leu Ser His Val
20 25 30
Phe Phe Lys Gln Met
35

<210> 33

<211> 101

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 33

Leu Phe Arg Leu Leu Leu Gln Tyr His Asp Pro Glu Leu Cys Asn His
1 5 10 15
Leu Asp Thr Lys Lys Cys Thr Pro Asp Met Tyr Thr Leu Asn Trp Phe
20 25 30
Gly Ser Leu Phe Ala Ser Cys Cys Ser Thr Glu Val Cys His Ala Leu
35 40 45
Trp Asp Leu Tyr Ile Gln Gln Ala Asp Pro Phe Met Val Phe Phe Leu
50 55 60
Ala Leu Ile Ile Leu Ile Asn Ala Lys Glu Glu Ile Leu Gln Met Lys
65 70 75 80
Ser Asp Ser Lys Glu Glu Val Ile Lys Phe Leu Glu Asn Met Pro Cys
85 90 95
Gln Leu Asn Ile Glu
100

<210> 34

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 34

Ile Val Asp Cys Arg Pro Ala Glu Gln Tyr Asn Ala Gly His Leu Ser
1 5 10 15
Thr Ala Phe His Leu
20

<210> 35

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 35
Val Ile His Arg Asn Ile Cys Pro Glu Ser Ile Leu Ile Thr Lys Arg
1 5 10 15
Gly Ser Trp Lys Leu Ala Gly Phe Asp Phe Cys Val Ser Ala Gln Asn
20 25 30
Pro Asn Asp Gln Glu Asn Tyr Phe Pro Cys His Tyr Glu Trp Asp Pro
35 40 45
Arg Ile Pro Pro Leu Pro Leu Gln Pro Asn Leu Asp Tyr Leu Ala Pro
50 55 60
Glu Tyr Val Thr Ser Ser Thr Cys Thr Val Gly Ser Ala Ser Asp Met
65 70 75 80
Phe Ser Leu Gly Cys Leu Ile Tyr Ala Ile Tyr Asn Gly Gly Lys Pro
85 90 95
Leu Ile Asp Ala Asn Asn Asn Asp Glu Tyr Lys Ser Asn Tyr Asn Lys
100 105 110
Tyr Met Asn Thr Leu Asn Ser Leu Thr His Glu Ser Met Asn Asn Leu
115 120 125
Pro Pro Glu Asn Leu Lys Glu Ser Leu Lys Arg Met Leu Ser Met Asp
130 135 140
Pro Thr Val Arg Pro Thr Ala Gln Glu Leu Thr Leu Ile Lys Tyr Phe
145 150 155 160

<210> 36

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 36

Asp Leu Leu Leu Gln Lys Thr Pro Pro Glu Asp Ile Lys Ser Asn Ile
1 5 10 15
Leu Pro Met Leu Tyr Tyr Ala Phe Glu Asp Ser Asp Ile Gln Ile Cys
20 25 30
Gln

<210> 37

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<221> VARIANT

<222> (1)...(261)

<223> Xaa = Any Amino Acid

<400> 37

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly Xaa Xaa Xaa Xaa
1 5 10 15
Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

[illegible]